

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/714712C
Source: FW16
Date Processed by STIC: 5-5-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 05/05/2005

PATENT APPLICATION: US/09/714,712C

TIME: 11:58:47

Input Set : A:\2nd Sub Seq List.txt

Output Set: N:\CRF4\05052005\I714712C.raw

5 <110> APPLICANT: Schmitz, Juergen
 6 Dzionek, Andrzej
 7 Buck, David William
 10 <120> TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS SPECIFIC FOR DENDRITIC CELLS
 COMPOSITIONS

11 AND METHODS OF USE THEREOF ANTIGENS RECOGNIZED THEREBY AND CELLS
 12 OBTAINED THEREBY

15 <130> FILE REFERENCE: 212302001100

18 <140> CURRENT APPLICATION NUMBER: US 09/714,712C

19 <141> CURRENT FILING DATE: 2000-11-15

21 <150> PRIOR APPLICATION NUMBER: US 60/197,205

22 <151> PRIOR FILING DATE: 2000-04-13

24 <150> PRIOR APPLICATION NUMBER: US 60/196,824

25 <151> PRIOR FILING DATE: 2000-04-11

27 <150> PRIOR APPLICATION NUMBER: US 60/180,775

28 <151> PRIOR FILING DATE: 2000-02-07

30 <150> PRIOR APPLICATION NUMBER: US 60/179,003

31 <151> PRIOR FILING DATE: 2000-01-28

33 <150> PRIOR APPLICATION NUMBER: US 60/167,076

34 <151> PRIOR FILING DATE: 1999-11-23

36 <150> PRIOR APPLICATION NUMBER: US 60/165,555

37 <151> PRIOR FILING DATE: 1999-11-15

40 <160> NUMBER OF SEQ ID NOS: 38

43 <170> SOFTWARE: PatentIn version 3.0

47 <210> SEQ ID NO: 1

48 <211> LENGTH: 1312

49 <212> TYPE: DNA

50 <213> ORGANISM: Homo sapiens

53 <220> FEATURE:

54 <221> NAME/KEY: misc_feature

55 <222> LOCATION: (1)..(1312)

56 <223> OTHER INFORMATION: BDCA-2 cDNA sequence

60 <400> SEQUENCE: 1

61 cagtgtattct cgtgcctcag cctcctgagt agccgaaatt acagacgtgt gccaccatgc 60
 63 ttggctaatt ttttgattt ttagtagaga tggggtttca ctatgttggc caggctagtc 120
 65 ttgaactcct ggcctgaagc aatccgcca cctcagcctc ccaaagtgt gagattatag 180
 67 gcacgagcca ctacacctgg ccacaaaatt ctttaaagaa gccaatccca tctcctcctca 240
 69 agagccaagg ggccacctca ccctcttggt acagcagatc ctgcctccac agtcaccctg 300
 71 ctcccaagtg caacctctgt ctgacctgc atggtgtgctg gtgccctcct gcctcaggcc 360
 73 gcgaagaagg atctaagggtc ttggcttggt tgaaagaacc acaccccgaa agtaacatct 420
 75 ttggagaaag tgatacaaga gcttctgcac ccacctgata gaggaagtc aaaggggtgtg 480
 77 cgcacacaca atggtgcctg aagaagagcc tcaagaccga gagaaaggac tctggtggtt 540
 79 ccagttgaag gtctggtcca tggcagtcgt atccatcttg ctcctcagtg tctgtttcac 600
 81 tgtgagttct gtggtgcctc acaattttat gtatagcaaa actgtcaaga ggctgtccaa 660

(ps.6)

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83 gttacgagag tatcaacagt atcatccaag cctgacctgc gtcattggaag gaaaggacat      720
85 agaagattgg agctgctgcc caacccttg gacttcattt cagtctagtt gctactttat      780
87 ttctactggg atgcaatctt ggactaagag tcaaaagaac tggtctgtga tgggggctga      840
89 tctggtggtg atcaacacca ggaagaaca ggatttcata attcagaatc tgaaaagaaa      900
91 ttcttcttat tttctggggc tgtcagatcc agggggctcg cgacattggc aatgggttga      960
93 ccagacacca tacaatgaaa atgtcacatt ctggcactca ggtgaaccca ataaccttga     1020
95 tgagcggtgt gcgataataa atttccgttc ttcagaagaa tggggctgga atgacattca     1080
97 ctgtcatgta cctcagaagt caatttgcaa gatgaagaag atctacatat aaatgaaata     1140
99 ttctccctgg aaatgtgttt gggttggcat ccaccgttgt agaaagctaa attgattttt     1200
101 taatttatgt gtaagttttg tacaaggaat gccctaaaaa tgtttcagca ggctgtcacc     1260
103 tattacactt atgatataat ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa           1312

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106 <210> SEQ ID NO: 2

107 <211> LENGTH: 213

108 <212> TYPE: PRT

109 <213> ORGANISM: Homo sapiens

112 <220> FEATURE:

113 <221> NAME/KEY: UNSURE

114 <222> LOCATION: (1)..(213)

115 <223> OTHER INFORMATION: amino acid sequence of one of the isoforms of BDCA-2 with
all six

116 exons expressed

120 <400> SEQUENCE: 2

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122 Met Val Pro Glu Glu Glu Pro Gln Asp Arg Glu Lys Gly Leu Trp Trp
123 1          5          10          15
125 Phe Gln Leu Lys Val Trp Ser Met Ala Val Val Ser Ile Leu Leu Leu
126          20          25          30
128 Ser Val Cys Phe Thr Val Ser Ser Val Val Pro His Asn Phe Met Tyr
129          35          40          45
131 Ser Lys Thr Val Lys Arg Leu Ser Lys Leu Arg Glu Tyr Gln Gln Tyr
132          50          55          60
134 His Pro Ser Leu Thr Cys Val Met Glu Gly Lys Asp Ile Glu Asp Trp
135 65          70          75          80
137 Ser Cys Cys Pro Thr Pro Trp Thr Ser Phe Gln Ser Ser Cys Tyr Phe
138          85          90          95
140 Ile Ser Thr Gly Met Gln Ser Trp Thr Lys Ser Gln Lys Asn Cys Ser
141          100         105         110
143 Val Met Gly Ala Asp Leu Val Val Ile Asn Thr Arg Glu Glu Gln Asp
144          115         120         125
146 Phe Ile Ile Gln Asn Leu Lys Arg Asn Ser Ser Tyr Phe Leu Gly Leu
147          130         135         140
149 Ser Asp Pro Gly Gly Arg Arg His Trp Gln Trp Val Asp Gln Thr Pro
150 145         150         155         160
152 Tyr Asn Glu Asn Val Thr Phe Trp His Ser Gly Glu Pro Asn Asn Leu
153          165         170         175
155 Asp Glu Arg Cys Ala Ile Ile Asn Phe Arg Ser Ser Glu Glu Trp Gly
156          180         185         190
158 Trp Asn Asp Ile His Cys His Val Pro Gln Lys Ser Ile Cys Lys Met
159          195         200         205
161 Lys Lys Ile Tyr Ile
162          210

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164 <210> SEQ ID NO: 3
165 <211> LENGTH: 1227
166 <212> TYPE: DNA
167 <213> ORGANISM: Mus musculus
170 <220> FEATURE:
171 <221> NAME/KEY: CDS
172 <222> LOCATION: (146)..(775)
173 <223> OTHER INFORMATION: coding sequence of mouse Dectin-2
177 <300> PUBLICATION INFORMATION:
179 <308> DATABASE ACCESSION NO: AF240357
180 <309> DATABASE ENTRY DATE: 2000-05-02
181 <313> RELEVANT RESIDUES: (1)..(1227)
184 <400> SEQUENCE: 3
185 cattggcccg ctctgtggca tttaactcaa gtgtgtgtgg aagttgattc tgaactctgg      60
187 cctcttttgac agaagccagg tccctgagtc gtatttttggg gacagatgca agaaaccctt      120
189 gaccttctga acatacacct caaca atg gtg cag gaa aga caa tcc caa ggg      172
190                               Met Val Gln Glu Arg Gln Ser Gln Gly
191                               1                               5
193 aag gga gtc tgc tgg acc ctg aga ctc tgg tca gct gct gtg att tcc      220
194 Lys Gly Val Cys Trp Thr Leu Arg Leu Trp Ser Ala Ala Val Ile Ser
195 10                               15                               20                               25
197 atg tta ctc ttg agt acc tgt ttc att gcg agc tgt gtg gtg act tac      268
198 Met Leu Leu Leu Ser Thr Cys Phe Ile Ala Ser Cys Val Val Thr Tyr
199                               30                               35                               40
201 caa ttt att atg gac cag ccc agt aga aga cta tat gaa ctt cac aca      316
202 Gln Phe Ile Met Asp Gln Pro Ser Arg Arg Leu Tyr Glu Leu His Thr
203                               45                               50                               55
205 tac cat tcc agt ctc acc tgc ttc agt gaa ggg act atg gtg tca gaa      364
206 Tyr His Ser Ser Leu Thr Cys Phe Ser Glu Gly Thr Met Val Ser Glu
207                               60                               65                               70
209 aaa atg tgg gga tgc tgc cca aat cac tgg aag tca ttt ggc tcc agc      412
210 Lys Met Trp Gly Cys Cys Pro Asn His Trp Lys Ser Phe Gly Ser Ser
211                               75                               80                               85
213 tgc tac ctc att tct acc aag gag aac ttc tgg agc acc agt gag cag      460
214 Cys Tyr Leu Ile Ser Thr Lys Glu Asn Phe Trp Ser Thr Ser Glu Gln
215 90                               95                               100                               105
217 aac tgt gtt cag atg ggg gct cat ctg gtg gtg atc aat act gaa gcg      508
218 Asn Cys Val Gln Met Gly Ala His Leu Val Val Ile Asn Thr Glu Ala
219                               110                               115                               120
221 gag cag aat ttc atc acc cag cag ctg aat gag tca ctt tct tac ttc      556
222 Glu Gln Asn Phe Ile Thr Gln Gln Leu Asn Glu Ser Leu Ser Tyr Phe
223                               125                               130                               135
225 ctg ggt ctt tcg gat cca caa ggt aat ggc aaa tgg caa tgg atc gat      604
226 Leu Gly Leu Ser Asp Pro Gln Gly Asn Gly Lys Trp Gln Trp Ile Asp
227                               140                               145                               150
229 gat act cct ttc agt caa aat gtc agg ttc tgg cac ccc cat gaa ccc      652
230 Asp Thr Pro Phe Ser Gln Asn Val Arg Phe Trp His Pro His Glu Pro
231                               155                               160                               165
233 aat ctt cca gaa gag cgg tgt gtt tca ata gtt tac tgg aat cct tcg      700

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234 Asn Leu Pro Glu Glu Arg Cys Val Ser Ile Val Tyr Trp Asn Pro Ser
235 170                      175                      180                      185
237 aaa tgg ggc tgg aat gat gtt ttc tgt gat agt aaa cac aat tca ata      748
238 Lys Trp Gly Trp Asn Asp Val Phe Cys Asp Ser Lys His Asn Ser Ile
239                      190                      195                      200
241 tgt gaa atg aag aag att tac cta tga gtgcctgtta ttcattaata      795
242 Cys Glu Met Lys Lys Ile Tyr Leu
243                      205
245 tctttaaagt tcagacctac caagaagcca taacttcttg gcctgtacat ctgacagagg      855
247 ccgttctttt cctagccact attctttact caaacagaat gagccctttc tccttctgat      915
249 ggtagagtt ttgtcaactt gacacaaact agagtcacct ggggagtagg atcttcagct      975
251 aaggaattgc ctctgtcagc ttgaccagtc agcatgtctg ggggcatttt cttgattaat      1035
253 gattgttgta agaggggtcca ggtggtaagc aaagggtgta aacccatgaa gagcaagcca      1095
255 gggagcatca tccatccatc tctgccctca ggtttctgcc ccaggggtctt gccttggttt      1155
257 ctttctatga actgctgtta cttgaaagta taagatgaat aaacaatttc atccaaaaaa      1215
259 aaaaaaaaaa aa      1227
262 <210> SEQ ID NO: 4
263 <211> LENGTH: 209
264 <212> TYPE: PRT
265 <213> ORGANISM: Mus musculus
268 <400> SEQUENCE: 4
270 Met Val Gln Glu Arg Gln Ser Gln Gly Lys Gly Val Cys Trp Thr Leu
271 1                      5                      10                      15
273 Arg Leu Trp Ser Ala Ala Val Ile Ser Met Leu Leu Leu Ser Thr Cys
274                      20                      25                      30
276 Phe Ile Ala Ser Cys Val Val Thr Tyr Gln Phe Ile Met Asp Gln Pro
277                      35                      40                      45
279 Ser Arg Arg Leu Tyr Glu Leu His Thr Tyr His Ser Ser Leu Thr Cys
280                      50                      55                      60
282 Phe Ser Glu Gly Thr Met Val Ser Glu Lys Met Trp Gly Cys Cys Pro
283 65                      70                      75                      80
285 Asn His Trp Lys Ser Phe Gly Ser Ser Cys Tyr Leu Ile Ser Thr Lys
286                      85                      90                      95
288 Glu Asn Phe Trp Ser Thr Ser Glu Gln Asn Cys Val Gln Met Gly Ala
289                      100                     105                     110
291 His Leu Val Val Ile Asn Thr Glu Ala Glu Gln Asn Phe Ile Thr Gln
292                      115                     120                     125
294 Gln Leu Asn Glu Ser Leu Ser Tyr Phe Leu Gly Leu Ser Asp Pro Gln
295                      130                     135                     140
297 Gly Asn Gly Lys Trp Gln Trp Ile Asp Asp Thr Pro Phe Ser Gln Asn
298 145                     150                     155                     160
300 Val Arg Phe Trp His Pro His Glu Pro Asn Leu Pro Glu Glu Arg Cys
301                      165                     170                     175
303 Val Ser Ile Val Tyr Trp Asn Pro Ser Lys Trp Gly Trp Asn Asp Val
304                      180                     185                     190
306 Phe Cys Asp Ser Lys His Asn Ser Ile Cys Glu Met Lys Lys Ile Tyr
307                      195                     200                     205
309 Leu
312 <210> SEQ ID NO: 5

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RAW SEQUENCE LISTING

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Input Set : A:\2nd Sub Seq List.txt

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313 <211> LENGTH: 237
314 <212> TYPE: PRT
315 <213> ORGANISM: Homo sapiens
318 <220> FEATURE:
319 <221> NAME/KEY: UNSURE
320 <222> LOCATION: (1)..(237)
321 <223> OTHER INFORMATION: amino acid sequence of human DCIR
324 <300> PUBLICATION INFORMATION:
325 <308> DATABASE ACCESSION NO: AJ133532
326 <309> DATABASE ENTRY DATE: 1999-09-01
327 <313> RELEVANT RESIDUES: (1)..(237)
330 <400> SEQUENCE: 5
332 Met Thr Ser Glu Ile Thr Tyr Ala Glu Val Arg Phe Lys Asn Glu Phe
333 1 5 10 15
335 Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg
336 20 25 30
338 Thr Ala Pro His Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
339 35 40 45
341 Ser Leu Leu Ile Phe Phe Leu Leu Ala Ile Ser Phe Phe Ile Ala
342 50 55 60
344 Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr
345 65 70 75 80
347 Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met
348 85 90 95
351 Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser
352 100 105 110
354 Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln
355 115 120 125
357 Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile
358 130 135 140
360 Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu
361 145 150 155 160
363 Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp
364 165 170 175
366 Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His
367 180 185 190
369 Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe
370 195 200 205
372 Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly
373 210 215 220
375 Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu
376 225 230 235
378 <210> SEQ ID NO: 6
379 <211> LENGTH: 5
380 <212> TYPE: PRT
381 <213> ORGANISM: Artificial Sequence
384 <220> FEATURE:
385 <223> OTHER INFORMATION: basic unit of a linking peptide
387 <400> SEQUENCE: 6

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/05/2005
PATENT APPLICATION: US/09/714,712C TIME: 11:58:48

Input Set : A:\2nd Sub Seq List.txt
Output Set: N:\CRF4\05052005\I714712C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; Xaa Pos. 1,2,4,5,6

VERIFICATION SUMMARY

DATE: 05/05/2005

PATENT APPLICATION: US/09/714,712C

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Input Set : A:\2nd Sub Seq List.txt

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L:800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0